



UNITED STATES PATENT AND TRADEMARK OFFICE

COMMISSIONER FOR PATENTS
UNITED STATES PATENT AND TRADEMARK OFFICE
WASHINGTON, DC 20231
www.uspto.gov

APPLICATION NO./ CONTROL NO.	FILING DATE JUN 17 2002	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.
---------------------------------	----------------------------	---	---------------------

09/604,325

COPY

EXAMINER

Bunner, B.

ART UNIT

PAPER

1647

8

DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 C.F.R. § 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 C.F.R. §§ 1.821-1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

APPLICANT IS GIVEN 30 days FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 C.F.R. §§ 1.821-1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 C.F.R. § 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 C.F.R. § 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Direct the response to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the response.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Bridget E. Bunner whose telephone number is (703) 305-7148. The examiner can normally be reached on 8:30-5 M-F.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Kunz can be reached at (703) 308-4623. The fax number for the organization where this application or proceeding is assigned is (703) 308-4242.

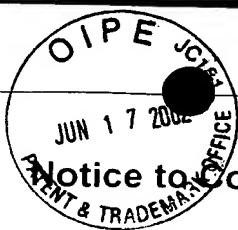
Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (703) 308-0196.

BEB
Art Unit 1647
11 February 2002

*Elizabeth C. Kimmner***RECEIVED**

JUN 25 2002

TECH CENTER 1600/2900



Application No.	Applicant(s)	
09/604,325	ZSEBO ET AL.	
Examiner	Art Unit	
Bridget E. Bunner	1647	

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other:

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

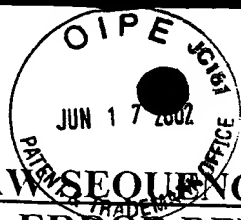
RECEIVED

JUN 25 2002

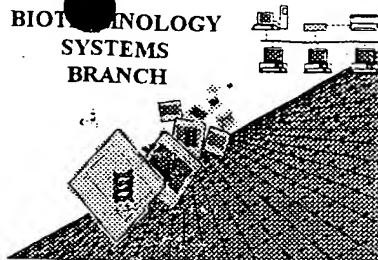
PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

TECH CENTER 1600/2900

B:
Bunneir



**RAW SEQUENCE LISTING
ERROR REPORT**



1647

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/604,325

Source: 1620 Russia

Date Processed by STIC: 8/10/2001

RECEIVED
AUG 20 2001
TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

RECEIVED

JUN 25 2002

TECH CENTER 1600/2900



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/604,325

DATE: 08/10/2001

TIME: 10:44:54

Input Set : A:\32953A.txt

Output Set: N:\CRF3\08102001\I604325.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Zsebo, Krisztina M.
7 Bosselman, Robert A.
8 Suggs, Sidney V.
9 Martin, Francis H.

11 (ii) TITLE OF INVENTION: Stem Cell Factor

13 (iii) NUMBER OF SEQUENCES: 104

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
17 (B) STREET: 6300 Sears Tower, 233 South Wacker Drive
18 (C) CITY: Chicago
19 (D) STATE: Illinois
20 (E) COUNTRY: United States of America
21 (F) ZIP: 60606-6402

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

29 (vi) CURRENT APPLICATION DATA:

30 (A) APPLICATION NUMBER: US/09/604,325
31 (B) FILING DATE: 26-Jun-2000
32 (C) CLASSIFICATION:

54 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: 08/449,649
36 (B) FILING DATE: 24-MAY-1995
39 (A) APPLICATION NUMBER: 07/982,255
40 (B) FILING DATE: 25-NOV-1992
43 (A) APPLICATION NUMBER: 07/589,701
44 (B) FILING DATE: 01-OCT-1990
47 (A) APPLICATION NUMBER: 07/573,616
48 (B) FILING DATE: 24-AUG-1990
51 (A) APPLICATION NUMBER: 07/537,198
52 (B) FILING DATE: 11-JUN-1990
55 (A) APPLICATION NUMBER: 07/422,383
56 (B) FILING DATE: 16-OCT-1989

58 (viii) ATTORNEY/AGENT INFORMATION:

59 (A) NAME: Clough, David W.
60 (B) REGISTRATION NUMBER: 36,107
61 (C) REFERENCE/DOCKET NUMBER: 01017/32953A

63 (ix) TELECOMMUNICATION INFORMATION:

64 (A) TELEPHONE: 312/474-6300
65 (B) TELEFAX: 312/474-0448
66 (C) TELEX:

68 (2) INFORMATION FOR SEQ ID NO: 1:

70 (i) SEQUENCE CHARACTERISTICS:

Does Not Comply
Corrected Diskette Needed

P3

RECEIVED

JUN 25 2002

TECH CENTER 1600/2900

RECEIVED

AUG 20 2001

TECH CENTER 1600/2900

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/604,325

DATE: 08/10/2001
TIME: 10:44:54

Input Set : A:\32953A.txt

Output Set: N:\CRF3\08102001\I604325.raw

71 (A) LENGTH: 165 amino acids
 72 (B) TYPE: amino acid
 73 (C) STRANDEDNESS: single
 74 (D) TOPOLOGY: linear
 76 (ii) MOLECULE TYPE: protein
 78 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 80 Glu Glu Ile Cys Arg Asn Pro Val Thr Asp Asn Val Lys Asp Ile Thr
 81 1 5 10 15
 83 Lys Leu Val Ala Asn Leu Pro Asn Asp Tyr Met Ile Thr Leu Asn Tyr
 84 20 25 30
 86 Val Ala Gly Met Asp Val Leu Pro Ser His Cys Trp Leu Arg Asp Met
 87 35 40 45
 89 Val Thr His Leu Ser Val Ser Leu Thr Thr Leu Leu Asp Lys Phe Ser
 90 50 55 60
 92 Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Gly
 93 65 70 75 80
 95 Lys Ile Val Asp Asp Leu Val Ala Cys Met Glu Glu Asn Ala Pro Lys
 96 85 90 95
 98 Asn Val Lys Glu Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro
 99 100 105 110
 101 Glu Glu Phe Phe Ser Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp
 102 115 120 125
 104 Phe Met Val Ala Ser Asp Thr Ser Asp Cys Val Leu Ser Ser Thr Leu
 105 130 135 140
 107 Gly Pro Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu
 108 145 150 155 160
 110 Pro Pro Val Ala Ala 165

113 (2) INFORMATION FOR SEQ ID NO: 2:

115 (i) SEQUENCE CHARACTERISTICS:

116 (A) LENGTH: 26 base pairs

117 (B) TYPE: nucleic acid

118 (C) STRANDEDNESS: single

119 (D) TOPOLOGY: linear

121 (ii) MOLECULE TYPE: DNA

123 (ix) FEATURE:

124 (A) NAME/KEY: modified_base

125 (B) LOCATION: 9

126 (D) OTHER INFORMATION: /mod_base= Inosine

128 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

130 ACRTTYTTNG GNGCRTTYTC YTCCAT

132 (2) INFORMATION FOR SEQ ID NO: 3:

134 (i) SEQUENCE CHARACTERISTICS:

135 (A) LENGTH: 23 base pairs

136 (B) TYPE: nucleic acid

137 (C) STRANDEDNESS: single

138 (D) TOPOLOGY: linear

140 (ii) MOLECULE TYPE: DNA

142 (ix) FEATURE:

26

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/604,325

DATE: 08/10/2001
TIME: 10:44:54

Input Set : A:\32953A.txt

Output Set: N:\CRF3\08102001\I604325.raw

143 (A) NAME/KEY: modified base
 144 (B) LOCATION: 11 & 14
 145 (D) OTHER INFORMATION: /mod_base= Inosine
 147 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 149 AARAAATCYT CNEGNETRAA RTT

151 (2) INFORMATION FOR SEQ ID NO: 4:
 153 (i) SEQUENCE CHARACTERISTICS:

154 (A) LENGTH: 14 base pairs
 155 (B) TYPE: nucleic acid
 156 (C) STRANDEDNESS: single
 157 (D) TOPOLOGY: linear

159 (ii) MOLECULE TYPE: DNA

161 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 163 GTYTCNGGYT TYTT

165 (2) INFORMATION FOR SEQ ID NO: 5:
 167 (i) SEQUENCE CHARACTERISTICS:

168 (A) LENGTH: 26 base pairs
 169 (B) TYPE: nucleic acid
 170 (C) STRANDEDNESS: single
 171 (D) TOPOLOGY: linear

173 (ii) MOLECULE TYPE: DNA

175 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 177 ATGGARGARA AYGCCCCCAA RAAYGT

179 (2) INFORMATION FOR SEQ ID NO: 6:
 181 (i) SEQUENCE CHARACTERISTICS:

182 (A) LENGTH: 20 base pairs
 183 (B) TYPE: nucleic acid
 184 (C) STRANDEDNESS: single
 185 (D) TOPOLOGY: linear

187 (ii) MOLECULE TYPE: DNA

189 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 191 CCNAAYGAYT AYATGWTMAC

193 (2) INFORMATION FOR SEQ ID NO: 7:
 195 (i) SEQUENCE CHARACTERISTICS:

196 (A) LENGTH: 20 base pairs
 197 (B) TYPE: nucleic acid
 198 (C) STRANDEDNESS: single
 199 (D) TOPOLOGY: linear

201 (ii) MOLECULE TYPE: DNA

203 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 205 GGNNGNARCA TRAANGGYTT

207 (2) INFORMATION FOR SEQ ID NO: 8:
 209 (i) SEQUENCE CHARACTERISTICS:

210 (A) LENGTH: 23 base pairs
 211 (B) TYPE: nucleic acid
 212 (C) STRANDEDNESS: single
 213 (D) TOPOLOGY: linear

215 (ii) MOLECULE TYPE: DNA

217 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

23

14

26

20

20

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/604,325

DATE: 08/10/2001

TIME: 10:44:54

Input Set : A:\32953A.txt

Output Set: N:\CRF3\08102001\I604325.raw

219 ACCAKAARAT CTTYAAANCG ATC

221 (2) INFORMATION FOR SEQ ID NO: 9: 23

223 (i) SEQUENCE CHARACTERISTICS:

224 (A) LENGTH: 22 base pairs

225 (B) TYPE: nucleic acid

226 (C) STRANDEDNESS: single

227 (D) TOPOLOGY: linear

OK 229 (ii) MOLECULE TYPE: DNA

231 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

233 GTATTTTCAA TAGATCCATT GA

235 (2) INFORMATION FOR SEQ ID NO: 10: 22

237 (i) SEQUENCE CHARACTERISTICS:

238 (A) LENGTH: 14 base pairs

239 (B) TYPE: nucleic acid

240 (C) STRANDEDNESS: single

241 (D) TOPOLOGY: linear

OK 243 (ii) MOLECULE TYPE: DNA

245 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

247 CCAACTATGT CGCC

249 (2) INFORMATION FOR SEQ ID NO: 11: 14

251 (i) SEQUENCE CHARACTERISTICS:

252 (A) LENGTH: 21 base pairs

253 (B) TYPE: nucleic acid

254 (C) STRANDEDNESS: single

255 (D) TOPOLOGY: linear

OK 257 (ii) MOLECULE TYPE: DNA

259 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

261 GTAGTCAAGC TGACTGATAA G

263 (2) INFORMATION FOR SEQ ID NO: 12: 21

265 (i) SEQUENCE CHARACTERISTICS:

266 (A) LENGTH: 21 base pairs

267 (B) TYPE: nucleic acid

268 (C) STRANDEDNESS: single

269 (D) TOPOLOGY: linear

OK 271 (ii) MOLECULE TYPE: DNA

273 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

275 TAACCAACAA TGACTAGGCA A

277 (2) INFORMATION FOR SEQ ID NO: 13: 21

279 (i) SEQUENCE CHARACTERISTICS:

280 (A) LENGTH: 16 base pairs

281 (B) TYPE: nucleic acid

282 (C) STRANDEDNESS: single

283 (D) TOPOLOGY: linear

OK 285 (ii) MOLECULE TYPE: DNA

287 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

289 TTCCAGAGTC AGTGTC

291 (2) INFORMATION FOR SEQ ID NO: 14: 16

293 (i) SEQUENCE CHARACTERISTICS:

294 (A) LENGTH: 29 base pairs

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/604,325

DATE: 08/10/2001

TIME: 10:44:54

Input Set : A:\32953A.txt

Output Set: N:\CRF3\08102001\I604325.raw

295 (B) TYPE: nucleic acid
 296 (C) STRANDEDNESS: single
 297 (D) TOPOLOGY: linear
 OK> 299 (ii) MOLECULE TYPE: DNA
 301 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
 303 GCGAAGCTTG CCTTCCTTA TGAAGAAGA 29
 305 (2) INFORMATION FOR SEQ ID NO: 15:
 307 (i) SEQUENCE CHARACTERISTICS:
 308 (A) LENGTH: 38 base pairs
 309 (B) TYPE: nucleic acid
 310 (C) STRANDEDNESS: single
 311 (D) TOPOLOGY: linear
 OK> 313 (ii) MOLECULE TYPE: DNA
 315 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
 317 GCGCCGCGGT TACGGTGGTA ACATGAAGGG CTTTGTGA 38
 319 (2) INFORMATION FOR SEQ ID NO: 16:
 321 (i) SEQUENCE CHARACTERISTICS:
 322 (A) LENGTH: 21 base pairs
 323 (B) TYPE: nucleic acid
 324 (C) STRANDEDNESS: single
 325 (D) TOPOLOGY: linear
 OK> 327 (ii) MOLECULE TYPE: DNA
 329 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 331 GATAAATGCA AGTGATAATC C 21
 333 (2) INFORMATION FOR SEQ ID NO: 17:
 335 (i) SEQUENCE CHARACTERISTICS:
 336 (A) LENGTH: 36 base pairs
 337 (B) TYPE: nucleic acid
 338 (C) STRANDEDNESS: single
 339 (D) TOPOLOGY: linear
 OK> 341 (ii) MOLECULE TYPE: DNA
 343 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
 345 GCGGTCGACC CGCGGAAGTT TAAGTCCATG CAACAC 36
 347 (2) INFORMATION FOR SEQ ID NO: 18:
 349 (i) SEQUENCE CHARACTERISTICS:
 350 (A) LENGTH: 36 base pairs
 351 (B) TYPE: nucleic acid
 352 (C) STRANDEDNESS: single
 353 (D) TOPOLOGY: linear
 OK> 355 (ii) MOLECULE TYPE: DNA
 357 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:
 359 CACCCGCGGT TATGCAACAG GGGGTAACAT AAATGG 36
 361 (2) INFORMATION FOR SEQ ID NO: 19:
 363 (i) SEQUENCE CHARACTERISTICS:
 364 (A) LENGTH: 36 base pairs
 365 (B) TYPE: nucleic acid
 366 (C) STRANDEDNESS: single
 367 (D) TOPOLOGY: linear
 wOL> 369 (ii) MOLECULE TYPE: DNA

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/604,325

DATE: 08/10/2001

TIME: 10:44:55

Input Set : A:\32953A.txt

Output Set: N:\CRF3\08102001\I604325.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:121 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=2
L:140 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:159 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4
L:173 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5
L:187 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6
L:201 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7
L:215 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8
L:229 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9
L:243 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10
L:257 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11
L:271 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=12
L:285 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=13
L:299 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=14
L:313 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=15
L:327 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=16
L:341 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=17
L:355 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=18
L:369 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=19
L:383 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=20
L:397 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=21
L:411 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=22
L:425 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=23
L:439 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24
L:453 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25
L:467 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26
L:481 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27
L:495 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=28
L:509 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=29
L:523 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=30
L:537 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=31
L:551 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=32
L:565 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=33
L:579 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=34
L:593 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=35
L:607 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=36
L:621 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=37
L:635 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=38
L:649 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=39
L:1441 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=47
L:1700 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 47
L:2770 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64
L:2800 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2803 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2868 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:2898 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72
L:2934 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/604,325

DATE: 08/10/2001

TIME: 10:44:55

Input Set : A:\32953A.txt

Output Set: N:\CRF3\08102001\I604325.raw

L:2952 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75
L:3000 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:78
L:3104 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=84
L:3118 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=85
L:3132 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=86
L:3146 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=87
L:3160 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=88
L:3174 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=89
L:3188 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=90
L:3202 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=91
L:3216 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=92
L:3230 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=93
L:3248 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:94
L:3280 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=96